



SEQUENCE LISTING

#7/a
CHK
8-6-99

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Lester, Henry A.
Davidson, Norman
Kofuji, Paulo
- 10 (ii) TITLE OF INVENTION: INWARD RECTIFIER, G-PROTEIN ACTIVATED,
MAMMALIAN, POTASSIUM CHANNELS AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 2
- 15 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
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(C) CITY: San Francisco
(D) STATE: California
20 (E) COUNTRY: United States
(F) ZIP: 94111-4187
- (v) COMPUTER READABLE FORM:
25 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: US 09/039,927
(B) FILING DATE: 16-MAR-1998
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: US 08/066,371
(B) FILING DATE: 21-MAR-1993
- (vii) PRIOR APPLICATION DATA:
40 (A) APPLICATION NUMBER: US 08/614,801
(B) FILING DATE: 07-MAR-1996
- (viii) ATTORNEY/AGENT INFORMATION:
45 (A) NAME: Trecartin, Richard F.
(B) REGISTRATION NUMBER: 31,801
(C) REFERENCE/DOCKET NUMBER: A-63098-1/RFT
- (ix) TELECOMMUNICATION INFORMATION:
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(C) TELEX: 910 277299

(2) INFORMATION FOR SEQ ID NO:1:

- 55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2076 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 60 (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
(A) NAME/KEY: CDS
65 (B) LOCATION: 32..1534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	GGCACGAGAA TCTGGATCTC CCCTCCGTAT T ATG TCT GCA CTC CGA AGG AAA	52
	Met Ser Ala Leu Arg Arg Lys	
5	1 5	
	TTT GGG GAC GAT TAC CAG GTA GTG ACC ACT TCG TCC AGC GGT TCG GGC	100
	Phe Gly Asp Asp Tyr Gln Val Val Thr Thr Ser Ser Ser Gly Ser Gly	
	10 15 20	
10	TTG CAG CCC CAG GGG CCA GGA CAG GGC CCA CAG CAG CAG CTT GTA CCC	148
	Leu Gln Pro Gln Gly Pro Gly Gln Gly Pro Gln Gln Gln Leu Val Pro	
	25 30 35	
15	AAG AAG AAA CGG CAG CGG TTC GTG GAC AAG AAC GGT CGG TGC AAT GTG	196
	Lys Lys Lys Arg Gln Arg Phe Val Asp Lys Asn Gly Arg Cys Asn Val	
	40 45 50 55	
	CAG CAC GGC AAC CTG GGC AGC GAG ACC AGT CGC TAC CTT TCC GAC CTC	244
20	Gln His Gly Asn Leu Gly Ser Glu Thr Ser Arg Tyr Leu Ser Asp Leu	
	60 65 70	
	TTC ACT ACC CTG GTG GAT CTC AAG TGG CGT TGG AAC CTC TTT ATC TTC	292
	Phe Thr Thr Leu Val Asp Leu Lys Trp Arg Trp Asn Leu Phe Ile Phe	
25	75 80 85	
	ATC CTC ACC TAC ACC GTG GCC TGG CTC TTC ATG GCG TCC ATG TGG TGG	340
	Ile Leu Thr Tyr Thr Val Ala Trp Leu Phe Met Ala Ser Met Trp Trp	
	90 95 100	
30	GTG ATC GCT TAT ACC CGG GGC GAC CTG AAC AAA GCC CAT GTC GGC AAC	388
	Val Ile Ala Tyr Thr Arg Gly Asp Leu Asn Lys Ala His Val Gly Asn	
	105 110 115	
35	TAC ACT CCC TGT GTG GCC AAT GTC TAT AAC TTC CCC TCT GCC TTC CTT	436
	Tyr Thr Pro Cys Val Ala Asn Val Tyr Asn Phe Pro Ser Ala Phe Leu	
	120 125 130 135	
	TTC TTC ATC GAG ACC GAG GCC ACC ATC GGC TAT GGC TAC CGC TAC ATC	484
40	Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly Tyr Gly Tyr Arg Tyr Ile	
	140 145 150	
	ACC GAC AAG TGC CCC GAG GGC ATC ATC CTT TTC CTT TTC CAG TCC ATC	532
45	Thr Asp Lys Cys Pro Glu Gly Ile Ile Leu Phe Leu Phe Gln Ser Ile	
	155 160 165	
	CTT GGC TCC ATC GTG GAC GCT TTC CTC ATC GGC TGC ATG TTC ATC AAG	580
	Leu Gly Ser Ile Val Asp Ala Phe Leu Ile Gly Cys Met Phe Ile Lys	
	170 175 180	
50	ATG TCC CAG CCC AAA AAG CGC GCC GAG ACC CTC ATG TTT AGC GAG CAT	628
	Met Ser Gln Pro Lys Lys Arg Ala Glu Thr Leu Met Phe Ser Glu His	
	185 190 195	
55	GCG GTT ATT TCC ATG AGG GAC GGA AAA CTC ACT CTC ATG TTC CGG GTG	676
	Ala Val Ile Ser Met Arg Asp Gly Lys Leu Thr Leu Met Phe Arg Val	
	200 205 210 215	
	GGC AAC CTG CGC AAC AGC CAC ATG GTC TCC GCG CAG ATC CGC TGC AAG	724
60	Gly Asn Leu Arg Asn Ser His Met Val Ser Ala Gln Ile Arg Cys Lys	
	220 225 230	
	CTG CTC AAA TCT CGG CAG ACA CCT GAG GGT GAG TTT CTA CCC CTT GAC	772
65	Leu Leu Lys Ser Arg Gln Thr Pro Glu Gly Glu Phe Leu Pro Leu Asp	
	235 240 245	

	CAA	CTT	GAA	CTG	GAT	GTA	GGT	TTT	AGT	ACA	GGG	GCA	GAT	CAA	CTT	TTT	820
	Gln	Leu	Glu	Leu	Asp	Val	Gly	Phe	Ser	Thr	Gly	Ala	Asp	Gln	Leu	Phe	
			250					255					260				
5	CTT	GTG	TCC	CCT	CTC	ACC	ATT	TGC	CAC	GTG	ATC	GAT	GCC	AAA	AGC	CCC	868
	Leu	Val	Ser	Pro	Leu	Thr	Ile	Cys	His	Val	Ile	Asp	Ala	Lys	Ser	Pro	
		265					270					275					
10	TTT	TAT	GAC	CTA	TCC	CAG	CGA	AGC	ATG	CAA	ACT	GAA	CAG	TTC	GAG	GTG	916
	Phe	Tyr	Asp	Leu	Ser	Gln	Arg	Ser	Met	Gln	Thr	Glu	Gln	Phe	Glu	Val	
	280					285					290					295	
	GTC	GTC	ATC	CTG	GAA	GGC	ATC	GTG	GAA	ACC	ACA	GGG	ATG	ACT	TGT	CAA	964
	Val	Val	Ile	Leu	Glu	Gly	Ile	Val	Glu	Thr	Thr	Gly	Met	Thr	Cys	Gln	
15					300					305					310		
	GCT	CGA	ACA	TCA	TAC	ACC	GAA	GAT	GAA	GTT	CTT	TGG	GGT	CAT	CGT	TTT	1012
	Ala	Arg	Thr	Ser	Tyr	Thr	Glu	Asp	Glu	Val	Leu	Trp	Gly	His	Arg	Phe	
				315					320					325			
20	TTC	CCT	GTA	ATT	TCT	TTA	GAA	GAA	GGA	TTC	TTT	AAA	GTC	GAT	TAC	TCC	1060
	Phe	Pro	Val	Ile	Ser	Leu	Glu	Glu	Gly	Phe	Phe	Lys	Val	Asp	Tyr	Ser	
		330					335						340				
25	CAG	TTC	CAT	GCA	ACC	TTT	GAA	GTC	CCC	ACC	CCT	CCG	TAC	AGT	GTG	AAA	1108
	Gln	Phe	His	Ala	Thr	Phe	Glu	Val	Pro	Thr	Pro	Pro	Tyr	Ser	Val	Lys	
		345					350					355					
30	GAG	CAG	GAA	GAA	ATG	CTT	CTC	ATG	TCT	TCC	CCT	TTA	ATA	GCA	CCA	GCC	1156
	Glu	Gln	Glu	Glu	Met	Leu	Leu	Met	Ser	Ser	Pro	Leu	Ile	Ala	Pro	Ala	
	360					365					370					375	
	ATA	ACC	AAC	AGC	AAA	GAA	AGA	CAC	AAT	TCT	GTG	GAG	TGC	TTA	GAT	GGA	1204
	Ile	Thr	Asn	Ser	Lys	Glu	Arg	His	Asn	Ser	Val	Glu	Cys	Leu	Asp	Gly	
35					380					385					390		
	CTA	GAT	GAC	ATT	AGC	ACA	AAA	CTT	CCA	TCG	AAG	CTG	CAG	AAA	ATT	ACG	1252
	Leu	Asp	Asp	Ile	Ser	Thr	Lys	Leu	Pro	Ser	Lys	Leu	Gln	Lys	Ile	Thr	
				395					400					405			
40	GGG	AGA	GAA	GAC	TTT	CCC	AAA	AAA	CTC	CTG	AGG	ATG	AGT	TCT	ACA	ACT	1300
	Gly	Arg	Glu	Asp	Phe	Pro	Lys	Lys	Leu	Leu	Arg	Met	Ser	Ser	Thr	Thr	
			410				415						420				
45	TCA	GAA	AAA	GCC	TAT	AGT	TTG	GGT	GAT	TTG	CCC	ATG	AAA	CTC	CAA	CGA	1348
	Ser	Glu	Lys	Ala	Tyr	Ser	Leu	Gly	Asp	Leu	Pro	Met	Lys	Leu	Gln	Arg	
		425					430					435					
50	ATA	AGT	TCG	GTT	CCT	GGC	AAC	TCT	GAA	GAA	AAA	CTG	GTA	TCT	AAA	ACC	1396
	Ile	Ser	Ser	Val	Pro	Gly	Asn	Ser	Glu	Glu	Lys	Leu	Val	Ser	Lys	Thr	
	440																

CAGAGGACTC TTCATTGAAG TGTGTTACT GTGTTGAACA TGAGTTACAA AGGGAGGACA 1714
 TCATAAGAAA GCTAATAGTT GGCATGTATT ATCACATCAA GCATGCAATA ATGTGCAAAT 1774
 5 TTTGCATTTA GTTTTCTGGC ATGATTTATA TATGGCATAT TTATATTGAA TATTCTGGAA 1834
 AAATATATAA ATATATATTT GAAGTGGAGA TATTCTCCCC ATAATTTCTA ATATATGTAT 1894
 TAAGCCAAAC ATGAGTGGAT AGCTTTCAGG GCACTAAAAT AATATACATG CATACATACA 1954
 10 TACATGCATA TGCACAGACA CATAACACA CATACTCATA TATATAAAAC ATACCCATAC 2014
 AAACATATAT ATCTAATAAA AATTGTGATG TTTTGTTCAG AAAAAAATAA AAAAACTCG 2074
 15 AG 2076

(2) INFORMATION FOR SEQ ID NO:2:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 501 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

30 Met Ser Ala Leu Arg Arg Lys Phe Gly Asp Asp Tyr Gln Val Val Thr
 1 5 10 15
 Thr Ser Ser Ser Gly Ser Gly Leu Gln Pro Gln Gly Pro Gly Gln Gly
 20 25 30
 35 Pro Gln Gln Gln Leu Val Pro Lys Lys Lys Arg Gln Arg Phe Val Asp
 35 40 45
 Lys Asn Gly Arg Cys Asn Val Gln His Gly Asn Leu Gly Ser Glu Thr
 50 55 60
 40 Ser Arg Tyr Leu Ser Asp Leu Phe Thr Thr Leu Val Asp Leu Lys Trp
 65 70 75 80
 Arg Trp Asn Leu Phe Ile Phe Ile Leu Thr Tyr Thr Val Ala Trp Leu
 45 85 90 95
 Phe Met Ala Ser Met Trp Trp Val Ile Ala Tyr Thr Arg Gly Asp Leu
 100 105 110
 50 Asn Lys Ala His Val Gly Asn Tyr Thr Pro Cys Val Ala Asn Val Tyr
 115 120 125
 Asn Phe Pro Ser Ala Phe Leu Phe Phe Ile Glu Thr Glu Ala Thr Ile
 55 130 135 140
 Gly Tyr Gly Tyr Arg Tyr Ile Thr Asp Lys Cys Pro Glu Gly Ile Ile
 145 150 155 160
 60 Leu Phe Leu Phe Gln Ser Ile Leu Gly Ser Ile Val Asp Ala Phe Leu
 165 170 175
 Ile Gly Cys Met Phe Ile Lys Met Ser Gln Pro Lys Lys Arg Ala Glu
 180 185 190
 65 Thr Leu Met Phe Ser Glu His Ala Val Ile Ser Met Arg Asp Gly Lys
 195 200 205

[illegible]